

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BRACCO, Laurent
SCHWEIGHOFFER, Fabien
TOCQUE, Bruno
- (ii) TITLE OF INVENTION: CONDITIONAL EXPRESSION SYSTEM
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Rhone-Poulenc Rorer Inc.
 - (B) STREET: 500 Arcola Road, Mailstop 3C43
 - (C) CITY: Collegeville
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19426
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: FR 95/03841
 - (B) FILING DATE: 31-MAR-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO PCT/FR96/00477
 - (B) FILING DATE: 29-MAR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Fehlner Esq., Paul F.
 - (B) REGISTRATION NUMBER: 35,135
 - (C) REFERENCE/DOCKET NUMBER: ST95021-US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (610) 454-3839
 - (B) TELEFAX: (610) 454-3808

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTCTATCAC TGATAGGGA

19

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TATCACCGCA AGGGATA

17

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Lys Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg
1 5 10 15

Glu Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys
20 25 30

Asp Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser
35 40 45

His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu
50 55 60

Met Phe Lys Thr Glu Gly Pro Asp Ser Asp
65 70

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 768 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | |
|---|-----|
| TTACTCGCGG CCCAGCCGGC CATGGCCCAG GTGCAGCTGC AGCAGTCTGG GGCAGAGCTT | 60 |
| GTAAGGTCAG GGGCCTCAGT CAAGTTGTCC TGCACAGCTT CTGGCTTCAA CATTAAAGAC | 120 |
| TACTATATGC ACTGGGTGAA GCAGAGGCCT GAACAGGGCC TGGAGTGGAT TGGATGGATT | 180 |
| GATCCTAAGA ATGGTGATAC TGAATATGCC CCGAAGTTCC AGGGCAAGGC CACTATGACT | 240 |
| GCAGACACAT CCTCCAATAC AGCCTACCTG CAGCTCAGCA GCCTGGCATC TGAGGACACT | 300 |
| GCCGTGTATT ATTGTAATTT TTACGGGGAT GCTTTGGACT ATTGGGGCCA AGGGACCACG | 360 |
| GTCACCGTCT CCTCAGGTGG AGGCGGTTCA GCGCGAGGTG GCTCTGGCGG TGGCGGATCG | 420 |
| GATGTTTTGA TGACCCAAAC TCCACTCACT TTGTCGGTTA CCATTGGACA ACCAGCCTCC | 480 |
| ATCTCTTGCA AGTCAAGTCA GAGCCTCTTG GATAGTGATG GAAAAACATA TTTGAATTGG | 540 |
| TTGTTACAGA GGCCAGGCCA GTCTCCAAAG CGCCTAATCT ATCTGGTGTC TAAACTGGAC | 600 |
| TCTGGAGTCC CTGACAGGTT CACTGGCAGT GGATCAGGGA CAGATTTTAC ACTTAAAATC | 660 |
| AACAGAGTGG AGGCTGAGGA TTTGGGAGTT TATTATTGCT GGCAAGGTAC ACATTCTCCG | 720 |
| CTTACGTTTC GTGCTGGCAC CAAGCTGGAA ATTAAACGGG CGGCCGCA | 768 |

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCC AAG CCC AGT ACC CCC CCA GGT TCT TCA
 Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser
 1 5 10

30

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG AAC CGG CTG GGC AAG
 Met Asn Arg Leu Gly Lys
 15

18

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asn Arg Leu Gly Lys
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
10 15

33

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Pro Lys Lys Lys Arg Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCTCTAGAC CCAAGCCCAG TACCCCCCA GGTCTTCAA CGCGTGGATC CATGTCCAGA 60
TTAGATAAAA GTAAAG 76

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGTACGGAAT TCGGGCCCTT ACTCGAGGGA CCCACTTTCA CATTTAAGTT G 51

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCTCTAGAC CCAAGCCCAG TACCCCCCA GGTTC'TTCAA CGCGTGGATC CATGGAACAA 60

CGCATAACCC TGAAAG 76

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGTACGGAAT TCGGGCCCTT ACTCGAGTGC TGT'TGTTTTT TTGTTACTCG G 51

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAGGCCATGG CATGAAGAAA CCACTGGATG GAGAA 35

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGTCGGATCC TCTAGATGCG GCCGCGTCTG AGTCAGGCCC TTC

43

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAGGCTCGAG AAGAAACCAC TGGATGGAGA A

31

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGGCTCGAG CCCAAGCCCA GTACCCCCC AGGTTCTTCA AAGAAACCAC TGGATGGAGA

60

A

61

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGTCGAATTC GGGCCCTCAG TCTGAGTCAG GCCCTTC

37

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAGGCCATGG AGGAGCCGCA GTCAGATCC

29

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGTCGGATCC TCTAGATGCG GCCGCCACGG GGGGAGCAGC CTCTGG

46

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Arg | Ile | Thr | Leu | Lys | Asp | Tyr | Ala | Met | Arg | Phe | Gly | Gln |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Lys | Thr | Ala | Lys | Asp | Leu | Gly | Val | Tyr | Gln | Ser | Ala | Ile | Asn | Lys |
| | | | 20 | | | | 25 | | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ile | His | Ala | Gly | Arg | Lys | Ile | Phe | Leu | Thr | Ile | Asn | Ala | Asp | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Tyr | Ala | Glu | Glu | Val | Lys | Pro | Phe | Pro | Ser | Asn | Lys | Lys | Thr |
| | 50 | | | | | | 55 | | | | 60 | | | | |

Thr Ala
65

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATCCTATCA CCGCAAGGGA TAA

23

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATAGTGGCG TTCCCTATTT CGA

23

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATCCGACTT TCACTTTTCT CTATCACTGA TAGTGAGTGG TAAACTCA

48

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCTTGAGTT TACCACTCCC TATCAGTGAT AGAGAAAAGT GAAAGTCG

48

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCCGACTT TCACTTTTCT CTATCACTGA TAGTGAGTGG TAAACTCACT AGGCTCAAAG

60

TGAAAAGAGA TAGTGACTAT CACTCACCAT TTGAGT

96